

<!--StartFragment--> ALIGNMENTS

RESULT 1
 Q4W8A9_9CAUL
 ID Q4W8A9_9CAUL Unreviewed; 257 AA.
 AC Q4W8A9;
 DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2005, sequence version 1.
 DT 05-FEB-2008, entry version 11.
 DE Carotenoid C2-hydroxylase.
 GN Name=crtG;
 OS Brevundimonas sp. SD212.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
 OC Caulobacteraceae; Brevundimonas.
 OX NCBI_TaxID=281067;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=SD212;
 RX PubMed=16085816; DOI=10.1128/AEM.71.8.4286-4296.2005;
 RA Nishida Y., Adachi K., Kazai H., Shizuri Y., Shindo K., Sawabe A.,
 RA Komemushi S., Miki W., Misawa N.;
 RT "Elucidation of a carotenoid biosynthesis gene cluster encoding a
 RT novel enzyme, 2,2'-beta-hydroxylase, from Brevundimonas sp. strain
 RT SD212 and combinatorial biosynthesis of new or rare xanthophylls."
 RL Appl. Environ. Microbiol. 71:4286-4296(2005).
 CC
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC
 DR EMBL; AB181388; BAD99415.1; -; Genomic_DNA.
 DR GO; GO:0003824; Fc catalytic activity; IEA:InterPro.
 DR GO; GO:0008152; P:metabolic process; IEA:InterPro.
 DR InterPro; IPR006088; Sterol_desatur.
 DR Pfam; PF01598; Sterol_desat; 1.
 PE 4: Predicted;
 SQ SEQUENCE 257 AA; 28641 MW; 35F465E7EC8A125C CRC64;

Query Match 100.0%; Score 1391; DB 2; Length 257;
 Best Local Similarity 100.0%; Pred. No. 1.4e-109;
 Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLRDLLTTLALSIIGLRYLLVGAAGHLLWAGAGRGRALNLRPPAMKRIRAEIVASLI 60
 |||||||
 Db 1 MLRDLLTTLALSIIGLRYLLVGAAGHLLWAGAGRGRALNLRPPAMKRIRAEIVASLI 60

Qy 61 ACPIYALPAALVLELWKRGGTAIYSDPDAWPLWLPVSLIVYLLAHDAFYVWVHRLHHP 120
 |||||||
 Db 61 ACPIYALPAALVLELWKRGGTAIYSDPDAWPLWLPVSLIVYLLAHDAFYVWVHRLHHP 120

Qy 121 RVFGWAHAEHHRSRDPASFASFAFDPAEAAATAWFPLALIVPIHWGVALTLLTMSLT 180
 |||||||
 Db 121 RVFGWAHAEHHRSRDPASFASFAFDPAEAAATAWFPLALIVPIHWGVALTLLTMSLT 180

Qy 181 AALNHAGREVWPAAWLERAPLRLWLTATHHDKRFGNGYGLYFQFWDRWAGTEVSAAP 240
 |||||||
 Db 181 AALNHAGREVWPAAWLERAPLRLWLTATHHDKRFGNGYGLYFQFWDRWAGTEVSAAP 240

Qy 241 SPPSPVIPPERPSAPL 257
 |||||||
 Db 241 SPPSPVIPPERPSAPL 257

RESULT 2
 Q0GXS3_9CAUL
 ID Q0GXS3_9CAUL Unreviewed; 257 AA.
 AC Q0GXS3;
 DT 03-OCT-2006, integrated into UniProtKB/TrEMBL.
 DT 03-OCT-2006, sequence version 1.
 DT 05-FEB-2008, entry version 8.
 DE 2,2'-beta-ionone ring hydroxylase.
 GN Name=crtG;
 OS Brevundimonas aurantiaca.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
 OC Caulobacteraceae; Brevundimonas.
 OX NCBI_TaxID=74316;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 15266;
 RX PubMed=16781830; DOI=10.1016/j.gene.2006.04.017;
 RA Tao L., Rouviere P.E., Cheng Q.;
 RT "A carotenoid synthesis gene cluster from a non-marine Brevundimonas
 that synthesizes hydroxylated astaxanthin.";
 RL Gene 379:101-108(2006).
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; DQ497427; ABF50965.1; -; Genomic_DNA.
 DR GO; GO:0003824; F:catalytic activity; IEA:InterPro.
 DR GO; GO:0008152; P:metabolic process; IEA:InterPro.
 DR InterPro; IPR006088; Sterol_desatur.
 DR Pfam; PF01598; Sterol_desat; 1.
 PE 4: Predicted;
 SQ SEQUENCE 257 AA; 28653 MW; 5FE010220DF75FE1 CRC64;

 Query Match 98.4%; Score 1369; DB 2; Length 257;
 Best Local Similarity 98.8%; Pred. No. 1.1e-107;
 Matches 254; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

 Qy 1 MLRDLLITTLALSLIIGLRYLLVGAAAHGLLWAGAGRGRALNLRPPAMKRIRAEIVASLI 60
 |||||||
 Db 1 MLRDLLITTLALSLIIGLRYLLVGAAAHGLLWAGAGRGRALNLRPPAMKRIRAEIVASLI 60
 |||||||
 Qy 61 ACPIYALPAALVLELWKRGGTAIYSDPDAWPLWWLPVSLIVYLLAHDAFYVWHRALHHP 120
 |||||||
 Db 61 ACPIYALPAALVLELWKRGGTAIYSDPHAWPLWWLPVSLIVYLLAHDAFYVWHRALHHP 120
 |||||||
 Qy 121 RVFGWAHAEHHRSRDPASFASFAFDPAEAAATAWFLPALALIVPIHVGVALTLLTMSLT 180
 |||||||
 Db 121 RVFGWAHAEHHRSRDPASFASFAFDPAEAAATAWFLPALALIVPIHVGVALTLLTMSLT 180
 |||||||
 Qy 181 AALNHAGREVWPAAWLERAPLRLWLTATHHDAHKRFNGNYGLYFQFWDRWAGTEVSAAP 240
 |||||||
 Db 181 AALNHAGSEVWPAAWLERAPLRLWLTATHHDAHKRFNGNYGLYFQFWDRWAGTEVSAAP 240
 |||||||
 Qy 241 SPPSPVIPPERPSAPL 257
 | |||||||
 Db 241 SRPSPVIPPERPSAPL 257
 <!--EndFragment-->